

XX AAD07141:
XX 24-OCF-2001 (first entry)
XX
XX Human CRIM1 protein.
XX
XX CRIM-1: Human; human chromosome 2p21-16.3; ophthalmological;
XX neuroprotective; renal; osteopathic; dental; vulnerrary; immunogen;
XX antibody; gene therapy; neurodegenerative disease; eye disorder;
XX cataract; bone morphogenic protein; BMG; renal disease; bone abnormality;
XX tooth abnormality; wound; S52.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..17
XX Domain 1..901
XX /label= "Signal_peptide"
XX /label= "Ectodomain"
XX /note= "This sequence is specifically claimed in claim
XX 15"
XX Protein 18..1036
XX /label= "Mature_CRIM1"
XX Region 200..207
XX /note= "Conserved N-terminal motif"
XX Region 336..391
XX /label= "CR_1"
XX /note= "Cysteine rich repeat"
XX Region 403..456
XX /label= "CR_2"
XX /note= "Cysteine rich repeat"
XX Misc-difference 414
XX /note= "Encoded by GAC"
XX Region 608..662
XX /label= "CR_3"
XX /note= "Cysteine rich repeat"
XX Region 679..734
XX /label= "CR_4"
XX /note= "Cysteine rich repeat"
XX Region 753..808
XX /label= "CR_5"
XX /note= "Cysteine rich repeat"
XX Region 819..873
XX /label= "CR_6"
XX /note= "Cysteine rich repeat"
XX
XX WO200138519-A1.
XX
XX 31-MAY-2001.
XX
XX 24-NOV-2000; 2000WO-AUD01435.
XX
XX 26-NOV-1999; 99AU-0004348.
XX (UYOU) UNTY QUEENSLAND.
XX
XX Little M, Yamada T, Holmes G, Georgas K, Kolie G, Wilkinson L;
XX WPI; 2001-343951/36.
XX N-PSDB; NAS11601.
XX
XX Nucleic acids from human chromosome 2p21-16.3 and the encoded peptide,
XX useful for preventing, diagnosing and treating e.g. eye disease,
XX especially cataract formation -
XX
XX
XX Claim 11: Fig 1; 169pp; English.
XX
XX The invention relates to nucleic acids from human chromosome 2p21-16.3
XX and the encoded peptide (and mouse and chicken orthologues) that
XX comprises a pGECPLP group, an insulin-like growth factor binding protein
XX (IGFBP)-like domain, cysteine-rich domains, an RGD (undefined) group
XX and a transmembrane domain. The protein, e.g. CRIM1, interacts with

CC peptides of the transforming growth factor superfamily. A composition
CC comprising an expression construct comprising the nucleic acids of the
CC invention or a mimetic which antagonises or mimics an activity of a CRIM1
CC polypeptide may be used in a method for modulating the biological
CC activity of a polypeptide of the bone morphogenic protein (BMP) family.
CC In this way they may be used to prevent or treat an eye disease,
CC especially cataract formation. They may also be used to treat
CC neurodegenerative diseases, renal and kidney disease, bone and tooth
CC abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in
CC gene therapy by using antibodies directed against CRIM1 polypeptides.
CC The present sequence represents human CRIM1 (AKA S52).
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XX Sequence 1036 AA:
XX
XX
XX Query Match 99.1%; Score 5901; DB 22; Length 1036;
XX Best Local Similarity 99.2%; Pred. No. 0;
XX Matches 1028; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 MYLVADRGAGCGHLLVSLGLLLPARSGTRALVCLPDCSKCEPRNRPGSTIVGVC 60
XX 1 MYLVADRGAGCGHLLVSLGLLLPARSGTRALVCLPDCSKCEPRNRPGSTIVGVC 60
XX 61 GCCYTCASQGNESCGGTGIGTCDRGKRCVIRPLNGSLIEYAGVCEDEMTDQLL 120
XX 61 GCCYTCASQGNESCGGTGIGTCDRGKRCVIRPLNGSLIEYAGVCEDEMTDQLL 120
XX 121 GFKPCNENLIAGCNTINRCGNTIFGCSNPFEPSPDMCLSKRIEERKPDCKARCE 180
XX 121 GFKPCNENLIAGCNTINRCGNTIFGCSNPFEPSPDMCLSKRIEERKPDCKARCE 180
XX 181 VQSPRCPEDESVLIEGAPFSGCPPLPSKVCNPAKGLKVCNPNLTVSKASGRGE 240
XX 181 VQSPRCPEDESVLIEGAPFSGCPPLPSKVCNPAKGLKVCNPNLTVSKASGRGE 240
XX 241 CCCLYECKPFVGVDCRTVCEPTVQOTACPDPSYETQVRLNADCCLTLPKRCBLSGLGF 300
XX 241 CCCLYECKPFVGVDCRTVCEPTVQOTACPDPSYETQVRLNADCCLTLPKRCBLSGLGF 300
XX 241 CCCLYECKPFVGVDCRTVCEPTVQOTACPDPSYETQVRLNADCCLTLPKRCBLSGLGF 300
XX 301 PFCVSGSTPRIVRSGDPTGKCCDVFECVNTKPCVFNVEYDDMDMNCFRRCQ 360
XX 301 PFCVSGSTPRIVRSGDPTGKCCDVFECVNTKPCVFNVEYDDMDMNCFRRCQ 360
XX 361 GGVAICTACCGELNCRIVYVBSGCCVCEDPYPPNNAGCTANGLLIAGDWRRED 420
XX 361 GGVAICTACCGELNCRIVYVBSGCCVCEDPYPPNNAGCTANGLLIAGDWRRED 420
XX 421 CTFQCVNGERHCVATVCGQCTPNFVKVPSGCCVCEPTIITVDPACGELSNCTLRK 480
XX 421 CTFQCVNGERHCVATVCGQCTPNFVKVPSGCCVCEPTIITVDPACGELSNCTLRK 480
XX 481 DCINGFKRDHNGRCQCTINTOELSEKRGCTLNCPEFGLTDAONCEIDECPRPKCR 540
XX 481 DCINGFKRDHNGRCQCTINTOELSEKRGCTLNCPEFGLTDAONCEIDECPRPKCR 540
XX 541 PTDCKYCPGLILKNKHGDDICRCKKPELSCSKICPLGPODSHGCLICKEASASAG 600
XX 541 PTDCKYCPGLILKNKHGDDICRCKKPELSCSKICPLGPODSHGCLICKEASASAG 600
XX 601 PTLISGTCITVDGHHKRNESWHDGRCYCLNGREKALTICVPAKGPYTHPQCCP 660
XX 601 PTLISGTCITVDGHHKRNESWHDGRCYCLNGREKALTICVPAKGPYTHPQCCP 660
XX 661 SCADDFVQKPELSTPSICHAPGGEYFVGEFTWINDSCQCTCHSGVLCETEVCPPLLC 720
XX 661 SCADDFVQKPELSTPSICHAPGGEYFVGEFTWINDSCQCTCHSGVLCETEVCPPLLC 720
XX 721 QNPSRTDSCPOCTDPPRPSLRNNSVYNNCKDEDDJFLAESKRPVYSCICIDS 780
XX 721 QNPSRTDSCPOCTDPPRPSLRNNSVYNNCKDEDDJFLAESKRPVYSCICIDS 780
XX 781 VISCSESCPSVSEPRVLKGGCCYCIKDTIPKVVGHFSKAYADDERMDLDSCTHC 840
XX 781 VISCSESCPSVSEPRVLKGGCCYCIKDTIPKVVGHFSKAYADDERMDLDSCTHC 840

XX WP1: 2001-343951/36.
DR N-PDB: AAS11602.

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especially cataract formation -

claim 11; Fig 1; 16pp; English.

The invention relates to nucleic acids from human chromosomes 2p21-16.3
and the encoded peptide (and mouse and chicken orthologues) that
comprises a pGECSP group, an insulin-like growth factor binding protein
(IGFBP)-like domain, cysteine-rich domains, an RGD (undefined) group
and a transmembrane domain. The protein, e.g. CRIM1, interacts with
peptides of the transforming growth factor superfamily. A composition
comprising an expression construct comprising the nucleic acids of the
invention or a mimetic which antagonises or mimics an activity of a CRIM1
polypeptide may be used in a method for modulating the biological
activity of a polypeptide of the bone morphogenic protein (BMP) family.
In this way they may be used to prevent or treat an eye disease,
especially cataract formation. They may also be used to treat
neurodegenerative diseases, renal and kidney disease, bone and tooth
abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in
gene therapy by using antibodies directed against CRIM1 polypeptides.
The present sequence represents mouse CRIM1 (AFA 552).

Sequence 1037 AA:

Query Match 90.8%; Score 5402.5; DB 22; Length 1037;
Best Local Similarity 88.5%; Pred. No. 6,7e+300;
Matches 918; Conservative 51; Mismatches 67; Indels 1; Gaps 1;

1 MYTVAGDGIAGGGCHLLVSLTGLILLPLSGSTRALVLCDDSKKEEPRNRPGSYGVG 60
DY IMLTVAGRGKLAGCGHLSVSLTLGLILLPLSGSTRALVLCDDSKKEEPRNRPGSYGVG 60
OY 1 MYTVAGRGKLAGCGHLSVSLTLGLILLPLSGSTRALVLCDDSKKEEPRNRPGSYGVG 60
DB 61 GCCTCAACGAGNCSGGTGTGTCGRCATCATTAPLNGSSTREYAVGCEDEMTDQILL 120
61 GCCTCAACGAGNCSGGTGTGTCGRCATCATTAPLNGSSTREYAVGCEDEMTDQILL 120
OY 61 GCCTCAACGAGNCSGGTGTGTCGRCATCATTAPLNGSSTREYAVGCEDEMTDQILL 120
DB 61 GCCTCAACGAGNCSGGTGTGTCGRCATCATTAPLNGSSTREYAVGCEDEMTDQILL 120
OY 121 GPCPCENILANGCNINMGKECTITPTCSNFPFSSODMCLSAKRIEEKPDCKSRKC 180
DB 121 GPCPCENILANGCNINMGKECTITPTCSNFPFSSODMCLSAKRIEEKPDCKSRKC 180
OY 121 GPCPCENILANGCNINMGKECTITPTCSNFPFSSODMCLSAKRIEEKPDCKSRKC 180
DB 121 GPCPCENILANGCNINMGKECTITPTCSNFPFSSODMCLSAKRIEEKPDCKSRKC 180
OY 181 YQSPSPCPEDSVLIETAPRGECCLPSCRYCNAAGLTAKVCOPGNILLYSKSGPE 240
DB 181 YQSPSPCPEDSVLIETAPRGECCLPSCRYCNAAGLTAKVCOPGNILLYSKSGPE 240
OY 181 YQSPSPCPEDSVLIETAPRGECCLPSCRYCNAAGLTAKVCOPGNILLYSKSGPE 240
DB 181 YQSPSPCPEDSVLIETAPRGECCLPSCRYCNAAGLTAKVCOPGNILLYSKSGPE 240
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DB 241 CGLIYACKRVGNCGRVBCPYVOQTACPAPPSYETOVLRLTAAGCCPIPBDCISGCF 300
OY 241 CGLIYACKRVGNCGRVBCPYVOQTACPAPPSYETOVLRLTAAGCCPIPBDCISGCF 300
DB 241 CGLIYACKRVGNCGRVBCPYVOQTACPAPPSYETOVLRLTAAGCCPIPBDCISGCF 300
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DB 301 PVEVGASTRIAYSKGDOTBKGCNDVFECYNDRKACYFNNAVETYDGDMFRNDNRFCQC 360
OY 301 PVEVGASTRIAYSKGDOTBKGCNDVFECYNDRKACYFNNAVETYDGDMFRNDNRFCQC 360
DB 301 PVEVGASTRIAYSKGDOTBKGCNDVFECYNDRKACYFNNAVETYDGDMFRNDNRFCQC 360
OY 361 GGVALFTQAGETINCERTYTPBGECPPCEDPVYFPNNPAGCIANGLLAHSRRAREDD 420
DB 361 GGVALFTQAGETINCERTYTPBGECPPCEDPVYFPNNPAGCIANGLLAHSRRAREDD 420
OY 361 GGVALFTQAGETINCERTYTPBGECPPCEDPVYFPNNPAGCIANGLLAHSRRAREDD 420
DB 361 GGVALFTQAGETINCERTYTPBGECPPCEDPVYFPNNPAGCIANGLLAHSRRAREDD 420
OY 421 CTFCGCCVNGERHCVAAYVGGTCTNPVKYVGBGCCVCEDEPTITVDPPACGELSNCTLTR 480
DB 421 CTFCGCCVNGERHCVAAYVGGTCTNPVKYVGBGCCVCEDEPTITVDPPACGELSNCTLTR 480
OY 421 CTFCGCCVNGERHCVAAYVGGTCTNPVKYVGBGCCVCEDEPTITVDPPACGELSNCTLTR 480
DB 421 CTFCGCCVNGERHCVAAYVGGTCTNPVKYVGBGCCVCEDEPTITVDPPACGELSNCTLTR 480
OY 481 DCINGRKRDHNHCRTCCINTDELCSERRKGCTINCEFGFLTDADONCEICRCRPBRKCR 540
DB 481 DCINGRKRDHNHCRTCCINTDELCSERRKGCTINCEFGFLTDADONCEICRCRPBRKCR 540
OY 481 DCINGRKRDHNHCRTCCINTDELCSERRKGCTINCEFGFLTDADONCEICRCRPBRKCR 540
DB 481 DCINGRKRDHNHCRTCCINTDELCSERRKGCTINCEFGFLTDADONCEICRCRPBRKCR 540
OY 541 PTWCDFCFGLGLKNKHGCDICRCKKCPBLSCSKICPLGFOODSHCCCLICRCREVPASG 600
DB 541 PTWCDFCFGLGLKNKHGCDICRCKKCPBLSCSKICPLGFOODSHCCCLICRCREVPASG 600